

#3

<110> U.S. Army Medical Research & Material Command

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626-A 067252.0107

<150> PCT/US00/12890

<151> 2000-05-12

<150> 09/611,419

<151> 2000-07-06

<150> 60/133,865

<151> 1999-05-12

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<151> 1993-09-21

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<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum
sequence

<221> CDS

<222> (13)...(1326)

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aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu 50 55 60	195
tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser 65 70 75	243
atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr 80 85 90	291
ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met 95 100 105	339
gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile 110 115 120 125	387
tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys 130 135 140	435
tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe 145 150 155	483
gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn 160 165 170	531
ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His 175 180 185	579
gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His 190 195 200 205	627
cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn 210 215 220	675
gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile 225 230 235	723
ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac	771

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Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
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ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg 867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
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act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc 915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
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atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac 963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
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Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
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ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct 1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
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ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa 1107
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tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag 1155
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gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac 1203
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aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa 1251
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<210> 2

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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum
sequence

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Ser	Arg	Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp
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Pro	Ile	Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys
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Asn	Phe	Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser
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Ile	Ser	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn
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Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu
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Gln	Asp	Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln
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Met	Ile	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile
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Thr	Asn	Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu
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Ile	Asp	Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn
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Asn	Ile	Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile
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Trp	Ile	Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu
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Ile	Lys	Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp
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Phe	Trp	Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn
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Asn	Ala	Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile
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Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn
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Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn
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385					390					395					400
Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser

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<220>
 <223> Synthetic construct based on Clostridium botulinum
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 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
 15 20 25

 tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat 147
 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 30 35 40 45

 ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa 195
 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
 50 55 60

 atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa 243
 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
 65 70 75

 aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc 291
 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
 80 85 90

 atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat 339
 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
 95 100 105

 tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg 387
 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
 110 115 120 125

 cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag 435
 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
 130 135 140

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Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile	
145 150 155	
acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg	531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu	
160 165 170	
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175 180 185	
aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc	627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile	
190 195 200 205	
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Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu	
210 215 220	
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Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp	
225 230 235	
ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat	771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn	
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270 275 280 285	
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Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys	
290 295 300	
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Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn	
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370 375 380	

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385 390 395	

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Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser	
400 405 410	

cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg	1299
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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum
sequence

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35 40 45	
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val	
50 55 60	
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser	
65 70 75 80	
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu	
85 90 95	
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Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr	
115 120 125	
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn	
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Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn	
145 150 155 160	
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln	
165 170 175	
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met	
180 185 190	
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys	

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Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr	
65 70 75	
gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac	291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn	
80 85 90	
tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac	339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn	
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aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act	387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr	
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Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr	
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160 165 170	
ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct	579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser	
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aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac	627
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Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys	
210 215 220	
gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa	723
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys	
225 230 235	
gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg	771
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu	
240 245 250	
aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc	819

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Arg	Gly	Tyr	Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr		
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Lys	Lys	Tyr	Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp		
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acc	aat	gct	tct	cag	gct	ggc	gta	gaa	aag	atc	ttg	tct	gct	ctg	gaa	1059	
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Ile	Pro	Asp	Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys		
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Asn	Asp	Gln	Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn		
				370					375					380			
aat	ggc	aac	gat	atc	ggc	ttc	atc	ggc	ttc	cac	cag	ttc	aac	aat	atc	1203	
Asn	Gly	Asn	Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile		
				385				390					395				
gct	aaa	ctg	gtt	gct	tcc	aac	tgg	tac	aat	cgt	cag	atc	gaa	cgt	tcc	1251	
Ala	Lys	Leu	Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser		
			400				405					410					
tct	cgc	act	ctg	ggc	tgc	tct	tgg	gag	ttc	atc	ccg	gtt	gat	gac	ggc	1299	
Ser	Arg	Thr	Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly		
			415			420					425						
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<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum sequence

Met 1	Ala	Ser	Thr	Phe 5	Thr	Glu	Tyr	Ile	Lys 10	Asn	Ile	Ile	Asn	Thr 15	Ser
Ile	Leu	Asn	Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg
			20					25					30		
Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile
			35				40					45			
Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu
						55					60				
Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe
65					70					75					80
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser
				85					90					95	
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly
			100					105					110		
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp
			115				120					125			
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile
					135						140				
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn
145					150					155					160
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp
				165						170				175	
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile
			180					185					190		
Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile
			195				200					205			
Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys
						215					220				
Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp
225					230					235				240	
Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr
				245					250				255		
Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr
			260					265					270		
Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr
			275				280					285			
Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr
						295					300				
Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr
305					310					315					320
Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala
				325						330				335	
Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp
			340					345					350		
Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln
</															

Arg Pro Leu

<210> 7

<211> 1341

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum
sequence

<221> CDS

<222> (10)...(1329)

<400> 7

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gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51
      Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile
          1             5             10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac    99
Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr
   15             20             25             30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac    147
Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn
          35             40             45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag    195
Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln
          50             55             60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc    243
Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser
          65             70             75

ttc tgg att cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac    291
Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr
          80             85             90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt    339
Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly
          95             100            105            110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat    387
Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp
          115            120            125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa    435
Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu
          130            135            140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat    483
Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn
          145            150            155

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aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat	531
Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn	
160 165 170	
acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc	579
Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile	
175 180 185 190	
ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa	627
Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys	
195 200 205	
tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa	675
Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu	
210 215 220	
cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt	723
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly	
225 230 235	
aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac	771
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn	
240 245 250	
aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc	819
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile	
255 260 265 270	
ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc	867
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg	
275 280 285	
gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct	915
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser	
290 295 300	
cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg	963
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu	
305 310 315	
gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac	1011
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr	
320 325 330	
ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc	1059
Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser	
335 340 345 350	
gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg	1107
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro	
355 360 365	
acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac	1155
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp	
370 375 380	
gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta	1203

Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
 385 390 395

ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag 1251
 Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
 400 405 410

gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag 1299
 Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
 415 420 425 430

ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc 1341
 Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
 435 440

<210> 8

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum
 sequence

<400> 8

Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1 5 10 15
 Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
 35 40 45
 Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
 50 55 60
 Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
 65 70 75 80
 Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
 85 90 95
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
 100 105 110
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
 115 120 125
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
 130 135 140
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
 145 150 155 160
 Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
 165 170 175
 Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
 180 185 190
 Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
 195 200 205
 Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
 210 215 220
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
 225 230 235 240

Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	
				245					250					255		
Ser	Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	
			260				265						270			
Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu	
		275				280					285					
Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser	
	290					295				300						
Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe	
305				310					315					320		
Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys	
			325					330						335		
Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu	
			340					345					350			
Leu	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr	
	355						360					365				
Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile	
	370					375					380					
Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu	
385				390				395						400		
Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val	
			405					410					415			
Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	
		420					425						430			
Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu									
	435						440									

<210> 9

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS

<222> (10)...(1359)

<400> 9

gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc	51
Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser	
1 5 10	
ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc	99
Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser	
15 20 25 30	
aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc	147
Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser	
35 40 45	
ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca	195
Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro	
50 55 60	

atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt	243
Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly	
65 70 75	
aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac	291
Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr	
80 85 90	
gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc	339
Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser	
95 100 105 110	
aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt	387
Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly	
115 120 125	
tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag	435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln	
130 135 140	
aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac	483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn	
145 150 155	
aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac	531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn	
160 165 170	
atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc	579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr	
175 180 185 190	
atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc	627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr	
195 200 205	
ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc	675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser	
210 215 220	
gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag	723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu	
225 230 235	
ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc	771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr	
240 245 250	
aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag	819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu	
255 260 265 270	
tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac	867
Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn	
275 280 285	

tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac	915
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn	
290 295 300	
gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac	963
Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp	
305 310 315	
acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac	1011
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn	
320 325 330	
aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac	1059
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp	
335 340 345 350	
aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc	1107
Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr	
355 360 365	
aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac	1155
Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn	
370 375 380	
act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag	1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu	
385 390 395	
aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt	1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly	
400 405 410	
ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt	1299
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly	
415 420 425 430	
aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc	1347
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val	
435 440 445	
cca gtc tcc gag taataggaat tc	1371
Pro Val Ser Glu	
450	

<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic construct based on Clostridium botulinum sequence

<400> 10

Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu

1	5	10	15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile			
	20	25	30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr			
	35	40	45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe			
	50	55	60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val			
65	70	75	80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser			
	85	90	95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu			
	100	105	110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser			
	115	120	125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu			
	130	135	140
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala			
145	150	155	160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met			
	165	170	175
Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys			
	180	185	190
Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu			
	195	200	205
Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn			
	210	215	220
Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp			
225	230	235	240
Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val			
	245	250	255
Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr			
	260	265	270
Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg			
	275	280	285
Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly			
	290	295	300
Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg			
305	310	315	320
Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys			
	325	330	335
Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His			
	340	345	350
Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp			
	355	360	365
Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr			
	370	375	380
Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile			
385	390	395	400
Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp			
	405	410	415
Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr			
	420	425	430
Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val			
	435	440	445
Ser Glu			
450			

<210> 11
 <211> 1374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on Clostridium botulinum
 sequence

<221> CDS
 <222> (10)...(1362)

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<400> 11
gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
      1             5             10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac 99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
    15             20             25             30

atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc 147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
      35             40             45

ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc 195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
      50             55             60

gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac 243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
      65             70             75

gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac 291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
      80             85             90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc 339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
      95             100            105            110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc 387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
      115            120            125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt 435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
      130            135            140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag 483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
      145            150            155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc 531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr

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160	165	170	
aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg			579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met			
175	180	185	190
aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac			627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp			
	195	200	205
ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag			675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu			
	210	215	220
aac atc gac gag aac cag atg ttg tgg att cgt gac ttc aac atc ttc			723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe			
	225	230	235
tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag			771
Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln			
	240	245	250
atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc			819
Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe			
	255	260	270
gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc			867
Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile			
	275	280	285
gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac ctg tcc			915
Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser			
	290	295	300
aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag			963
Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys			
	305	310	315
aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg			1011
Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met			
	320	325	330
ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc			1059
Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile			
	335	340	350
tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg			1107
Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu			
	355	360	365
aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc			1155
Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile			
	370	375	380
aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc			1203
Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser			
	385	390	395

ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt	1251
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg	
400 405 410	

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag	1299
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu	
415 420 425 430	

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac	1347
Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp	
435 440 445	

cca ggt tgg gtc gag taataggaat tc	1374
Pro Gly Trp Val Glu	
450	

<210> 12
 <211> 451
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12

Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro	
1 5 10 15	
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile	
20 25 30	
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln	
35 40 45	
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val	
50 55 60	
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe	
65 70 75 80	
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn	
85 90 95	
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile	
100 105 110	
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile	
115 120 125	
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly	
130 135 140	
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu	
145 150 155 160	
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys	
165 170 175	
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu	
180 185 190	
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp	
195 200 205	
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile	
210 215 220	
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys	
225 230 235 240	

Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
 245 250 255
 Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
 260 265 270
 Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
 275 280 285
 Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser Lys Leu
 290 295 300
 Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
 305 310 315 320
 Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
 325 330 335
 Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
 340 345 350
 Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
 355 360 365
 Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn
 370 375 380
 Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg
 385 390 395 400
 Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser
 405 410 415
 Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys
 420 425 430
 Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly
 435 440 445
 Trp Val Glu
 450

<210> 13
 <211> 1400
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on Clostridium botulinum
 sequence

<221> CDS
 <222> (10)...(1356)

<400> 13
 gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51
 Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
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 acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat 99
 Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15 20 25 30

 aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct 147
 Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
 35 40 45

 tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act 195
 Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr

50					55					60					
tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac	243														
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr															
65 70 75															
cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt tcc gag	291														
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu															
80 85 90															
gtc aac atc tct caa aac gac tac att atc tac gac aac aag tac aag	339														
Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys															
95 100 105 110															
aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag	387														
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys															
115 120 125															
atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac	435														
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp															
130 135 140															
aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg	483														
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp															
145 150 155															
acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac	531														
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr															
160 165 170															
ggt aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc	579														
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val															
175 180 185 190															
act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt	627														
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly															
195 200 205															
aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt	675														
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val															
210 215 220															
tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac	723														
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr															
225 230 235															
att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc	771														
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr															
240 245 250															
gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag	819														
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys															
255 260 265 270															
gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta	867														
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu															
275 280 285															

aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act	915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr	
290 295 300	
tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta	963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu	
305 310 315	
tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act	1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr	
320 325 330	
aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc	1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val	
335 340 345 350	
gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc	1107
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr	
355 360 365	
aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac	1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn	
370 375 380	
caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt	1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe	
385 390 395	
aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat	1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp	
400 405 410	
act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc	1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr	
415 420 425 430	
aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg	1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp	
435 440 445	
caa gaa aaa taatagggat ccgcggccgc acgcgtccccg ggactagtga	1396
Gln Glu Lys	
attc	1400
<210> 14	
<211> 449	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Synthetic Construct	
<400> 14	
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu	

1		5		10		15									
Asn	Asn	Ser	Ile	Pro	Phe	Lys	Leu	Ser	Ser	Tyr	Thr	Asp	Asp	Lys	Ile
			20					25					30		
Leu	Ile	Ser	Tyr	Phe	Asn	Lys	Phe	Phe	Lys	Arg	Ile	Lys	Ser	Ser	Ser
		35					40					45			
Val	Leu	Asn	Met	Arg	Tyr	Lys	Asn	Asp	Lys	Tyr	Val	Asp	Thr	Ser	Gly
	50					55					60				
Tyr	Asp	Ser	Asn	Ile	Asn	Ile	Asn	Gly	Asp	Val	Tyr	Lys	Tyr	Pro	Thr
65					70					75					80
Asn	Lys	Asn	Gln	Phe	Gly	Ile	Tyr	Asn	Asp	Lys	Leu	Ser	Glu	Val	Asn
			85					90					95		
Ile	Ser	Gln	Asn	Asp	Tyr	Ile	Ile	Tyr	Asp	Asn	Lys	Tyr	Lys	Asn	Phe
		100						105					110		
Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Asn	Tyr	Asp	Asn	Lys	Ile	Val
		115					120					125			
Asn	Val	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Arg	Asp	Asn	Asn
	130					135					140				
Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	His	Asn	Glu	Ile	Ile	Trp	Thr	Leu
145					150					155					160
Gln	Asp	Asn	Ala	Gly	Ile	Asn	Gln	Lys	Leu	Ala	Phe	Asn	Tyr	Gly	Asn
			165					170					175		
Ala	Asn	Gly	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile
		180						185				190			
Thr	Asn	Asp	Arg	Leu	Gly	Asp	Ser	Lys	Leu	Tyr	Ile	Asn	Gly	Asn	Leu
	195					200						205			
Ile	Asp	Gln	Lys	Ser	Ile	Leu	Asn	Leu	Gly	Asn	Ile	His	Val	Ser	Asp
	210				215						220				
Asn	Ile	Leu	Phe	Lys	Ile	Val	Asn	Cys	Ser	Tyr	Thr	Arg	Tyr	Ile	Gly
225					230				235						240
Ile	Arg	Tyr	Phe	Asn	Ile	Phe	Asp	Lys	Glu	Leu	Asp	Glu	Thr	Glu	Ile
			245					250				255			
Gln	Thr	Leu	Tyr	Ser	Asn	Glu	Pro	Asn	Thr	Asn	Ile	Leu	Lys	Asp	Phe
		260					265					270			
Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asp	Lys	Glu	Tyr	Tyr	Leu	Leu	Asn	Val
	275					280						285			
Leu	Lys	Pro	Asn	Asn	Phe	Ile	Asp	Arg	Arg	Lys	Asp	Ser	Thr	Leu	Ser
	290				295						300				
Ile	Asn	Asn	Ile	Arg	Ser	Thr	Ile	Leu	Leu	Ala	Asn	Arg	Leu	Tyr	Ser
305					310					315					320
Gly	Ile	Lys	Val	Lys	Ile	Gln	Arg	Val	Asn	Asn	Ser	Ser	Thr	Asn	Asp
			325					330				335			
Asn	Leu	Val	Arg	Lys	Asn	Asp	Gln	Val	Tyr	Ile	Asn	Phe	Val	Ala	Ser
		340					345					350			
Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr	Asn	Lys
	355					360						365			
Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn	Gln	Val
	370				375					380					
Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Lys	Asn
385					390				395						400
Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp	Thr	Val
			405					410				415			
Val	Ala	Ser	Thr	Trp	Tyr	Tyr	Thr	His	Met	Arg	Asp	His	Thr	Asn	Ser
		420					425					430			
Asn	Gly	Cys	Phe	Trp	Asn	Phe	Ile	Ser	Glu	Glu	His	Gly	Trp	Gln	Glu
		435					440					445			

Lys

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1305)

<400> 15

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gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
      1             5             10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac    99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
  15             20             25             30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc    147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
             35             40             45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga    195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
             50             55             60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac    243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
             65             70             75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc    291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
             80             85             90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc    339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
             95             100             105             110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg    387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
             115             120             125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat    435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
             130             135             140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac    483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
             145             150             155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac    531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
             160             165             170

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tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc	579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser	
175 180 185 190	
aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc	627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val	
195 200 205	
ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc	675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe	
210 215 220	
gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag	723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu	
225 230 235	
cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac	771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr	
240 245 250	
aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc	819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile	
255 260 265 270	
acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac	867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr	
275 280 285	
cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag	915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu	
290 295 300	
gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac	963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn	
305 310 315	
ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat	1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp	
320 325 330	
gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag	1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys	
335 340 345 350	
atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa	1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln	
355 360 365	
atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag	1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln	
370 375 380	
aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac	1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn	
385 390 395	

ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc	1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser	
400 405 410	

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag	1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln	
415 420 425 430	

gag aac taataggaat tc	1317
Glu Asn	

<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu	
1 5 10 15	
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn	
20 25 30	
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn	
35 40 45	
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr	
50 55 60	
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile	
65 70 75 80	
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile	
85 90 95	
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile	
100 105 110	
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr	
115 120 125	
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys	
130 135 140	
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn	
145 150 155 160	
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg	
165 170 175	
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu	
180 185 190	
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys	
195 200 205	
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr	
210 215 220	
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp	
225 230 235 240	
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys	
245 250 255	
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln	
260 265 270	
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys	

aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc	339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr	
95 100 105 110	
atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag	387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys	
115 120 125	
gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag	435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys	
130 135 140	
tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc	483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile	
145 150 155	
aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc	531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala	
160 165 170	
aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac	579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn	
175 180 185 190	
ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac	627
Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn	
195 200 205	
tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc	675
Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe	
210 215 220	
ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag	723
Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln	
225 230 235	
tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac	771
Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr	
240 245 250	
gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc	819
Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile	
255 260 265 270	
aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac	867
Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn	
275 280 285	
ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt	915
Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg	
290 295 300	
ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac	963
Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn	
305 310 315	
atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc	1011

Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser	
320 325 330	
gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag	1059
Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln	
335 340 345 350	
acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac	1107
Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp	
355 360 365	
gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag	1155
Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln	
370 375 380	
atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt	1203
Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly	
385 390 395	
aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac	1251
Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr	
400 405 410	
ttc tgt atc tcc cag tgg tac ctg cgt cgt atc tcc gag aac atc aac	1299
Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn	
415 420 425 430	
aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt	1347
Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly	
435 440 445	
tgg acc gag taataggaat tc	1368
Trp Thr Glu	

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18	
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn	
1 5 10 15	
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu	
20 25 30	
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val	
35 40 45	
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu	
50 55 60	
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser	
65 70 75 80	
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr	
85 90 95	

Asn	Asn	Asn	Asp	Ile	Gln	Thr	Tyr	Leu	Gln	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105						110	
Ser	Cys	Ile	Lys	Asn	Asp	Ser	Gly	Trp	Lys	Val	Ser	Ile	Lys	Gly	Asn
		115					120						125		
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Val	Asn	Ala	Lys	Ser	Lys	Ser	Ile
		130				135					140				
Phe	Phe	Glu	Tyr	Ser	Ile	Lys	Asp	Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Lys
145					150					155					160
Trp	Phe	Ser	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asn	Ala	Asn	Ile
			165					170						175	
Tyr	Ile	Asn	Gly	Ser	Leu	Lys	Lys	Ser	Glu	Lys	Ile	Leu	Asn	Leu	Asp
		180						185					190		
Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	Cys	Thr
		195					200						205		
Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	Gly	Arg
	210					215					220				
Glu	Leu	Asn	Ala	Thr	Glu	Val	Ser	Ser	Leu	Tyr	Trp	Ile	Gln	Ser	Ser
225					230					235					240
Thr	Asn	Thr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	Asp	Thr
			245					250						255	
Gln	Tyr	Tyr	Leu	Phe	Asn	Gln	Gly	Met	Gln	Asn	Ile	Tyr	Ile	Lys	Tyr
		260					265						270		
Phe	Ser	Lys	Ala	Ser	Met	Gly	Glu	Thr	Ala	Pro	Arg	Thr	Asn	Phe	Asn
		275				280					285				
Asn	Ala	Ala	Ile	Asn	Tyr	Gln	Asn	Leu	Tyr	Leu	Gly	Leu	Arg	Phe	Ile
	290					295					300				
Ile	Lys	Lys	Ala	Ser	Asn	Ser	Arg	Asn	Ile	Asn	Asn	Asp	Asn	Ile	Val
305					310					315					320
Arg	Glu	Gly	Asp	Tyr	Ile	Tyr	Leu	Asn	Ile	Asp	Asn	Ile	Ser	Asp	Glu
			325					330						335	
Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	Thr	Gln
		340						345					350		
Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	Val	Leu
		355					360					365			
Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	Ile	Leu
	370					375					380				
Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	Lys	Phe
385					390					395					400
Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	Phe	Cys
			405					410					415		
Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	Lys	Leu
		420					425					430			
Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly	Trp	Thr
		435				440						445			

Glu

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS

<222> (1) ... (1239)

<400> 19

atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc	48
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe	
1 5 10 15	
ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa	96
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu	
20 25 30	
gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct	144
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser	
35 40 45	
ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa	192
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu	
50 55 60	
ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag	240
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln	
65 70 75 80	
ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac	288
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr	
85 90 95	
gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc	336
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe	
100 105 110	
gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct	384
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala	
115 120 125	
ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt	432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val	
130 135 140	
aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt	480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val	
145 150 155 160	
gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc	528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr	
165 170 175	
act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg	576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro	
180 185 190	
gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct	624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala	
195 200 205	
ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc	672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile	

210	215	220	
gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac			720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn			
225	230	235	240
aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac			768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn			
	245	250	255
gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct			816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala			
	260	265	270
aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct			864
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala			
	275	280	285
ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac			912
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr			
	290	295	300
aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat			960
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp			
305	310	315	320
gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac			1008
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn			
	325	330	335
atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct			1056
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser			
	340	345	350
atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg			1104
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu			
	355	360	365
aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc			1152
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile			
	370	375	380
ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act			1200
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr			
385	390	395	400
gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa			1242
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln			
	405	410	

<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

Met	Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe
1				5				10						15	
Phe	Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu
			20					25					30		
Glu	Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser
		35					40					45			
Leu	Asp	Leu	Ile	Gln	Gln	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	
50						55				60					
Pro	Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln
65					70					75					80
Leu	Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr
				85				90						95	
Glu	Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe
			100					105					110		
Glu	His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala
		115					120					125			
Leu	Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val
130						135					140				
Lys	Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val
145					150					155					160
Glu	Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr
				165				170						175	
Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro
			180					185					190		
Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala
		195					200					205			
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile
210					215						220				
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn
225					230					235					240
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn
				245					250					255	
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala
			260					265					270		
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala
		275					280					285			
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr
290					295						300				
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp
305					310					315					320
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn
				325					330					335	
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser
			340					345					350		
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu
		355					360					365			
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Arg	Asp	Asn	Tyr	Gly	Thr	Leu	Ile
370						375					380				
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr
385					390					395					400
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln			
				405					410						

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1) ... (1239)

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<400> 21
atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc 48
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
1 5 10 15

atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga 96
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
20 25 30

atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc 144
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
35 40 45

aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca 192
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
50 55 60

tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc 240
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65 70 75 80

tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc 288
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
85 90 95

atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac 336
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
100 105 110

atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag 384
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
115 120 125

gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc 432
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
130 135 140

gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat 480
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145 150 155 160

ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac 528
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
165 170 175

atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac 576

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Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn		
			180					185					190				
gag	acc	gcc	aag	ggt	aac	ttc	gag	aac	gct	ttc	gag	atc	gct	ggt	gcc	624	
Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala		
		195					200					205					
tcc	atc	ttg	ttg	gag	ttc	atc	cca	gag	ttg	ttg	atc	cca	gtc	gtc	ggt	672	
Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly		
	210					215					220						
gcc	ttc	ttg	ttg	gag	tcc	tac	atc	gac	aac	aag	aac	aag	atc	atc	aag	720	
Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys		
225					230					235					240		
acc	atc	gac	aac	gct	ttg	acc	aag	aga	aac	gag	aag	tgg	tcc	gac	atg	768	
Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met		
			245						250					255			
tac	ggt	ttg	atc	gtc	gcc	caa	tgg	ttg	tcc	acc	gtc	aac	acc	caa	ttc	816	
Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe		
		260						265					270				
tac	acc	atc	aag	gag	ggt	atg	tac	aag	gcc	ttg	aac	tac	cag	gcc	caa	864	
Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln		
		275					280					285					
gct	ttg	gag	gag	atc	atc	aag	tac	aga	tac	aac	atc	tac	tcc	gag	aag	912	
Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys		
	290					295					300						
gag	aag	tcc	aac	att	aac	atc	gac	ttc	aac	gac	atc	aac	tcc	aag	ctg	960	
Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu		
305					310					315					320		
aac	gag	ggt	att	aac	cag	gcc	atc	gac	aac	atc	aac	aac	ttc	atc	aac	1008	
Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn		
				325					330					335			
ggt	tgt	tcc	gtc	tcc	tac	ttg	atg	aag	aag	atg	att	cca	ttg	gcc	gtc	1056	
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val		
			340					345					350				
gag	aag	ttg	ttg	gac	ttc	gac	aac	acc	ctg	aag	aag	aac	ttg	ttg	aac	1104	
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn		
		355					360					365					
tac	atc	gac	gag	aac	aag	ttg	tac	ttg	atc	ggt	tcc	gct	gag	tac	gag	1152	
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu		
	370					375					380						
aag	tcc	aag	gtc	aac	aag	tac	ttg	aag	acc	atc	atg	cca	ttc	gac	ttg	1200	
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu		
385					390					395					400		
tcc	atc	tac	acc	aac	gac	acc	atc	ttg	atc	gag	atg	ttc	taa			1242	
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe					

<210> 22
 <211> 413
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

Met	Ala	Pro	Gly	Ile	Cys	Ile	Asp	Val	Asp	Asn	Glu	Asp	Leu	Phe	Phe	1	5	10	15
Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser	Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg	20	25	30	
Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile	35	40	45	
Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro	50	55	60	
Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val	Asp	Val	Pro	Val	65	70	75	80
Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr	85	90	95	
Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp	100	105	110	
Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	115	120	125	
Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	130	135	140	
Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	145	150	155	160
Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	165	170	175	
Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	180	185	190	
Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	195	200	205	
Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	210	215	220	
Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	225	230	235	240
Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	245	250	255	
Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	260	265	270	
Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	275	280	285	
Ala	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	290	295	300	
Glu	Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	305	310	315	320
Asn	Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	325	330	335	
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	340	345	350	
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn				

	355		360		365										
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu
	370					375				380					
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu
385					390					395					400
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe			
				405					410						

<210> 23

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<221> CDS

<222> (1)...(1197)

<400> 23

atg	tcc	ctg	tac	aac	aag	acc	ctt	gac	tgt	aga	gag	ctg	ctg	gtg	aag	48
Met	Ser	Leu	Tyr	Asn	Lys	Thr	Leu	Asp	Cys	Arg	Glu	Leu	Leu	Val	Lys	
1				5					10					15		
aac	act	gac	ctg	cca	ttc	atc	ggt	gac	atc	agt	gac	gtg	aag	act	gac	96
Asn	Thr	Asp	Leu	Pro	Phe	Ile	Gly	Asp	Ile	Ser	Asp	Val	Lys	Thr	Asp	
			20					25					30			
atc	ttc	ctg	cgt	aag	gac	atc	aac	gag	gag	act	gag	gtg	atc	tac	tac	144
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr	
		35					40					45				
cca	gac	aac	gtg	tca	gta	gac	caa	gtg	atc	ctc	agt	aag	aac	acc	tcc	192
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser	
	50					55					60					
gag	cat	gga	caa	cta	gac	ctg	ctc	tac	cct	agt	atc	gac	agt	gag	agt	240
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser	
65					70				75					80		
gag	atc	ctg	cca	ggg	gag	aat	caa	gtc	ttc	tac	gac	aac	cgt	acc	cag	288
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln	
				85				90					95			
aac	gtg	gac	tac	ctg	aac	tcc	tac	tac	tac	cta	gag	tct	cag	aag	ctg	336
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu	
			100					105					110			
agt	gac	aac	gtg	gag	gac	ttc	act	ttc	acg	cgt	tca	atc	gag	gag	gct	384
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala	
		115					120					125				
ctg	gac	aac	agt	gca	aag	gtg	tac	act	tac	ttc	cct	acc	ctg	gct	aac	432
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn	
	130					135					140					

aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac	480
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn	
145 150 155 160	
gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg	528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu	
165 170 175	
gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca	576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala	
180 185 190	
ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc	624
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe	
195 200 205	
gca gtc act ggt gtc acc atc ctg ctg gag gca ttc cct gag ttc aca	672
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr	
210 215 220	
atc cct gct ctg ggt gca ttc gtg atc tac agt aag gtc cag gag cga	720
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg	
225 230 235 240	
aac gag atc atc aag acc atc gac aac tgt ctg gag cag agg atc aag	768
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys	
245 250 255	
aga tgg aag gac tcc tac gag tgg atg atg gga acg tgg ttg tcc agg	816
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg	
260 265 270	
atc atc acc cag ttc aac aac atc tcc tac cag atg tac gac tcc ctg	864
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu	
275 280 285	
aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag	912
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys	
290 295 300	
aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac	960
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn	
305 310 315 320	
ctg aag aac agt ctg gac gtc aag atc tgc gag gca atg aac aac atc	1008
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile	
325 330 335	
aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg	1056
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met	
340 345 350	
ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag	1104
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys	
355 360 365	
gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt	1152

Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
 370 375 380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac 1197
 Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
 385 390 395

taa 1200

<210> 24

<211> 399

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 24

Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1 5 10 15
 Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
 20 25 30
 Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
 35 40 45
 Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
 50 55 60
 Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
 65 70 75 80
 Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
 85 90 95
 Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
 100 105 110
 Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
 115 120 125
 Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
 130 135 140
 Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
 145 150 155 160
 Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
 165 170 175
 Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
 195 200 205
 Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
 210 215 220
 Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
 225 230 235 240
 Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
 245 250 255
 Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
 260 265 270
 Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
 275 280 285
 Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
 290 295 300
 Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn

305		310		315		320									
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile
		325							330					335	
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met
		340						345					350		
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys
		355					360				365				
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly
	370					375				380					
Glu	Val	Asp	Lys	Leu	Lys	Ala	Lys	Val	Asn	Asn	Ser	Phe	Gln	Asn	
385				390					395						

<210> 25
 <211> 1161
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1158)

<400> 25	
atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac	48
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn	
1 5 10 15	
aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc	96
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe	
20 25 30	
gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac	144
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp	
35 40 45	
aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac	192
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn	
50 55 60	
cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg	240
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu	
65 70 75 80	
aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac	288
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr	
85 90 95	
gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct	336
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser	
100 105 110	
aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg	384
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu	
115 120 125	

ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag	432
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys	
130 135 140	
ggt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag	480
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu	
145 150 155 160	
gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac	528
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp	
165 170 175	
aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg	576
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu	
180 185 190	
aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc	624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala	
195 200 205	
acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc	672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile	
210 215 220	
cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag	720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu	
225 230 235 240	
aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga	768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg	
245 250 255	
tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc	816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile	
260 265 270	
acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc	864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser	
275 280 285	
tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag	912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys	
290 295 300	
tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg	960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu	
305 310 315 320	
aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac	1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn	
325 330 335	
aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg	1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu	
340 345 350	
cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc	1104

Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
 355 360 365

gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag 1152
 Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
 370 375 380

gtt gac taa 1161
 Val Asp
 385

<210> 26
 <211> 386
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 26
 Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1 5 10 15
 Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20 25 30
 Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35 40 45
 Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50 55 60
 Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65 70 75 80
 Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85 90 95
 Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
 100 105 110
 Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
 115 120 125
 Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
 130 135 140
 Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
 145 150 155 160
 Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
 165 170 175
 Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
 180 185 190
 Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
 195 200 205
 Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
 210 215 220
 Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
 225 230 235 240
 Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
 245 250 255
 Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
 260 265 270
 Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
 275 280 285

Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
 290 295 300
 Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
 305 310 315 320
 Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
 325 330 335
 Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
 340 345 350
 Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
 355 360 365
 Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
 370 375 380
 Val Asp
 385

<210> 27
 <211> 1149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1146)

<400> 27
 atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct 48
 Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1 5 10 15
 tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att 96
 Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
 20 25 30
 gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag 144
 Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
 35 40 45
 gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag 192
 Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
 50 55 60
 aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac 240
 Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
 65 70 75 80
 tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac 288
 Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
 85 90 95
 gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac 336
 Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
 100 105 110
 gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag 384

Val	Asn	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu	Gln	Pro	Lys	
		115					120					125				
atc	tac	acc	ttc	ttc	tcc	tcc	gag	ttc	atc	aac	aac	gtc	aac	aag	cct	432
Ile	Tyr	Thr	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asn	Asn	Val	Asn	Lys	Pro	
		130				135					140					
gtg	cag	gcc	gca	ttg	ttc	gta	agc	tgg	att	cag	cag	gtg	tta	gta	gac	480
Val	Gln	Ala	Ala	Leu	Phe	Val	Ser	Trp	Ile	Gln	Gln	Val	Leu	Val	Asp	
		145			150					155					160	
ttc	act	act	gag	gct	aac	cag	aag	tcc	act	ggt	gac	aag	atc	gct	gac	528
Phe	Thr	Thr	Glu	Ala	Asn	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile	Ala	Asp	
				165					170					175		
atc	tcc	atc	gtc	gtc	cca	tac	atc	ggc	ctg	gct	ctg	aac	atc	ggc	aac	576
Ile	Ser	Ile	Val	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Ile	Gly	Asn	
			180					185					190			
gag	gca	cag	aag	ggc	aac	ttc	aag	gat	gcc	ctt	gag	ttg	ttg	ggc	gcc	624
Glu	Ala	Gln	Lys	Gly	Asn	Phe	Lys	Asp	Ala	Leu	Glu	Leu	Leu	Gly	Ala	
		195					200					205				
ggc	att	ttg	ttg	gag	ttc	gaa	ccc	gag	ctg	ctg	atc	cct	acc	atc	ctg	672
Gly	Ile	Leu	Leu	Glu	Phe	Glu	Pro	Glu	Leu	Leu	Ile	Pro	Thr	Ile	Leu	
		210				215					220					
gtc	ttc	acg	atc	aag	tcc	ttc	ctg	ggc	tcc	tcc	gac	aac	aag	aac	aag	720
Val	Phe	Thr	Ile	Lys	Ser	Phe	Leu	Gly	Ser	Ser	Asp	Asn	Lys	Asn	Lys	
					230					235					240	
gtc	att	aag	gcc	atc	aac	aac	gcc	ctg	aag	gag	cgt	gac	gag	aag	tgg	768
Val	Ile	Lys	Ala	Ile	Asn	Asn	Ala	Leu	Lys	Glu	Arg	Asp	Glu	Lys	Trp	
				245					250					255		
aag	gaa	gtc	tat	tcc	ttc	atc	gtc	tgc	aac	tgg	atg	acc	aag	atc	aac	816
Lys	Glu	Val	Tyr	Ser	Phe	Ile	Val	Ser	Asn	Trp	Met	Thr	Lys	Ile	Asn	
			260					265					270			
acc	cag	ttc	aac	aag	cga	aag	gag	cag	atg	tac	cag	gct	ctg	cag	aac	864
Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu	Gln	Asn	
		275					280					285				
cag	gtc	aac	gcc	atc	aag	acc	atc	atc	gag	tcc	aag	tac	aac	tcc	tac	912
Gln	Val	Asn	Ala	Ile	Lys	Thr	Ile	Ile	Glu	Ser	Lys	Tyr	Asn	Ser	Tyr	
		290				295					300					
acc	ctg	gag	gag	aag	aac	gag	ctt	acc	aac	aag	tac	gat	atc	aag	cag	960
Thr	Leu	Glu	Glu	Lys	Asn	Glu	Leu	Thr	Asn	Lys	Tyr	Asp	Ile	Lys	Gln	
		305			310					315					320	
atc	gag	aac	gag	ctg	aac	cag	aag	gtc	tcc	atc	gcc	atg	aac	aac	atc	1008
Ile	Glu	Asn	Glu	Leu	Asn	Gln	Lys	Val	Ser	Ile	Ala	Met	Asn	Asn	Ile	
				325					330					335		
gac	agg	ttc	ctg	acc	gag	tcc	tcc	atc	tcc	tac	ctg	atg	aag	ctc	atc	1056
Asp	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile	

340	345	350	
aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag			1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys			
355	360	365	
acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg			1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu			
370	375	380	
taa			1149
<210> 28			
<211> 382			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic Construct			
<400> 28			
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala			
1 5 10 15			
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile			
20 25 30			
Asp Asp Thr Val Thr Ser Asn Asn Tyr Glu Asn Asp Leu Asp Gln			
35 40 45			
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu			
50 55 60			
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp			
65 70 75 80			
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn			
85 90 95			
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn			
100 105 110			
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys			
115 120 125			
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro			
130 135 140			
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp			
145 150 155 160			
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp			
165 170 175			
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn			
180 185 190			
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala			
195 200 205			
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu			
210 215 220			
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys			
225 230 235 240			
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp			
245 250 255			
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn			
260 265 270			
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn			
275 280 285			

Gln	Val	Asn	Ala	Ile	Lys	Thr	Ile	Ile	Glu	Ser	Lys	Tyr	Asn	Ser	Tyr		
290						295					300						
Thr	Leu	Glu	Glu	Lys	Asn	Glu	Leu	Thr	Asn	Lys	Tyr	Asp	Ile	Lys	Gln		
305					310					315					320		
Ile	Glu	Asn	Glu	Leu	Asn	Gln	Lys	Val	Ser	Ile	Ala	Met	Asn	Asn	Ile		
				325					330					335			
Asp	Arg	Phe	Leu	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys	Leu	Ile		
		340						345					350				
Asn	Glu	Val	Lys	Ile	Asn	Lys	Leu	Arg	Glu	Tyr	Asp	Glu	Asn	Val	Lys		
	355					360					365						
Thr	Tyr	Leu	Leu	Asn	Tyr	Ile	Ile	Gln	His	Gly	Ser	Ile	Leu				
370					375						380						

<210> 29

<211> 1227

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<221> CDS

<222> (1)...(1224)

<400> 29

atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc	48
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe	
1 5 10 15	
ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct	96
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro	
20 25 30	
aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac	144
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn	
35 40 45	
ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att	192
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile	
50 55 60	
tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca	240
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro	
65 70 75 80	
aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt	288
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val	
85 90 95	
gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt	336
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly	
100 105 110	
gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa	384
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu	
115 120 125	

gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac	432
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn	
130 135 140	
aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc	480
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile	
145 150 155 160	
aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att	528
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile	
165 170 175	
gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc	576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile	
180 185 190	
att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg	624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu	
195 200 205	
gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc	672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val	
210 215 220	
att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag	720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys	
225 230 235 240	
aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct	768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala	
245 250 255	
aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga	816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg	
260 265 270	
att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg	864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu	
275 280 285	
caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac	912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn	
290 295 300	
aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc	960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile	
305 310 315 320	
aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag	1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys	
325 330 335	
aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag	1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys	
340 345 350	

ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac	1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His	
355 360 365	

gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg	1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu	
370 375 380	

gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac	1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn	
385 390 395 400	

tcc tcc att cca ttt gag ctt tct taa	1227
Ser Ser Ile Pro Phe Glu Leu Ser	
405	

<210> 30
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30															
Met	Ala	Pro	Pro	Arg	Leu	Cys	Ile	Arg	Val	Asn	Asn	Ser	Glu	Leu	Phe
1				5					10					15	
Phe	Val	Ala	Ser	Glu	Ser	Ser	Tyr	Asn	Glu	Asn	Asp	Ile	Asn	Thr	Pro
			20					25					30		
Lys	Glu	Ile	Asp	Asp	Thr	Thr	Asn	Leu	Asn	Asn	Asn	Tyr	Arg	Asn	Asn
			35				40					45			
Leu	Asp	Glu	Val	Ile	Leu	Asp	Tyr	Asn	Ser	Gln	Thr	Ile	Pro	Gln	Ile
	50					55					60				
Ser	Asn	Arg	Thr	Leu	Asn	Thr	Leu	Val	Gln	Asp	Asn	Ser	Tyr	Val	Pro
65					70					75					80
Arg	Tyr	Asp	Ser	Asn	Gly	Thr	Ser	Glu	Ile	Glu	Glu	Tyr	Asp	Val	Val
				85					90					95	
Asp	Phe	Asn	Val	Phe	Phe	Tyr	Leu	His	Ala	Gln	Lys	Val	Pro	Glu	Gly
			100					105					110		
Glu	Thr	Asn	Ile	Ser	Leu	Thr	Ser	Ser	Ile	Asp	Thr	Ala	Leu	Leu	Glu
		115					120					125			
Glu	Ser	Lys	Asp	Ile	Phe	Phe	Ser	Ser	Glu	Phe	Ile	Asp	Thr	Ile	Asn
	130					135					140				
Lys	Pro	Val	Asn	Ala	Ala	Leu	Phe	Ile	Asp	Trp	Ile	Ser	Lys	Val	Ile
145					150					155					160
Arg	Asp	Phe	Thr	Thr	Glu	Ala	Thr	Gln	Lys	Ser	Thr	Val	Asp	Lys	Ile
				165					170					175	
Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Val	Gly	Leu	Ala	Leu	Asn	Ile
			180					185					190		
Ile	Ile	Glu	Ala	Glu	Lys	Gly	Asn	Phe	Glu	Glu	Ala	Phe	Glu	Leu	Leu
		195					200					205			
Gly	Val	Gly	Ile	Leu	Leu	Glu	Phe	Val	Pro	Glu	Leu	Thr	Ile	Pro	Val
	210					215					220				
Ile	Leu	Val	Phe	Thr	Ile	Lys	Ser	Tyr	Ile	Asp	Ser	Tyr	Glu	Asn	Lys
225					230					235				240	
Asn	Lys	Ala	Ile	Lys	Ala	Ile	Asn	Asn	Ser	Leu	Ile	Glu	Arg	Glu	Ala

				245					250				255				
Lys	Trp	Lys	Glu	Ile	Tyr	Ser	Trp	Ile	Val	Ser	Asn	Trp	Leu	Thr	Arg		
			260					265					270				
Ile	Asn	Thr	Gln	Phe	Asn	Lys	Arg	Lys	Glu	Gln	Met	Tyr	Gln	Ala	Leu		
		275					280					285					
Gln	Asn	Gln	Val	Asp	Ala	Ile	Lys	Thr	Ala	Ile	Glu	Tyr	Lys	Tyr	Asn		
	290					295					300						
Asn	Tyr	Thr	Ser	Asp	Glu	Lys	Asn	Arg	Leu	Glu	Ser	Glu	Tyr	Asn	Ile		
305					310					315					320		
Asn	Asn	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Lys	Val	Ser	Leu	Ala	Met	Lys		
			325					330						335			
Asn	Ile	Glu	Arg	Phe	Met	Thr	Glu	Ser	Ser	Ile	Ser	Tyr	Leu	Met	Lys		
		340					345						350				
Leu	Ile	Asn	Glu	Ala	Lys	Val	Gly	Lys	Leu	Lys	Lys	Tyr	Asp	Asn	His		
	355					360						365					
Val	Lys	Ser	Asp	Leu	Leu	Asn	Tyr	Ile	Leu	Asp	His	Arg	Ser	Ile	Leu		
	370				375					380							
Gly	Glu	Gln	Thr	Asn	Glu	Leu	Ser	Asp	Leu	Val	Thr	Ser	Thr	Leu	Asn		
385				390					395						400		
Ser	Ser	Ile	Pro	Phe	Glu	Leu	Ser										
			405														

<210> 31
 <211> 1233
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (1)...(1230)

<400> 31																
atg	gcc	aaa	aat	acc	ggt	aaa	tct	gaa	cag	tgt	att	att	ggt	aat	aat	48
Met	Ala	Lys	Asn	Thr	Gly	Lys	Ser	Glu	Gln	Cys	Ile	Ile	Val	Asn	Asn	
1				5				10					15			
gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta																96
Glu	Asp	Leu	Phe	Phe	Ile	Ala	Asn	Lys	Asp	Ser	Phe	Ser	Lys	Asp	Leu	
		20				25						30				
gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa																144
Ala	Lys	Ala	Glu	Thr	Ile	Ala	Tyr	Asn	Thr	Gln	Asn	Asn	Thr	Ile	Glu	
		35				40					45					
aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt																192
Asn	Asn	Phe	Ser	Ile	Asp	Gln	Leu	Ile	Leu	Asp	Asn	Asp	Leu	Ser	Ser	
	50				55				60							
ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac																240
Gly	Ile	Asp	Leu	Pro	Asn	Glu	Asn	Thr	Glu	Pro	Phe	Thr	Asn	Phe	Asp	
65				70				75					80			
gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att																288
Asp	Ile	Asp	Ile	Pro	Val	Tyr	Ile	Lys	Gln	Ser	Ala	Leu	Lys	Lys	Ile	

85								90				95				
ttt	gtg	gat	gga	gat	agc	ctt	ttt	gaa	tat	tta	cat	gct	caa	aca	ttt	336
Phe	Val	Asp	Gly	Asp	Ser	Leu	Phe	Glu	Tyr	Leu	His	Ala	Gln	Thr	Phe	
			100							105				110		
cct	tct	aat	ata	gaa	aat	cta	caa	cta	acg	aat	tca	tta	aat	gat	gct	384
Pro	Ser	Asn	Ile	Glu	Asn	Leu	Gln	Leu	Thr	Asn	Ser	Leu	Asn	Asp	Ala	
		115					120						125			
tta	aga	aat	aat	aat	aaa	gtc	tat	act	ttt	ttt	tct	aca	aac	ctt	gtt	432
Leu	Arg	Asn	Asn	Asn	Lys	Val	Tyr	Thr	Phe	Phe	Ser	Thr	Asn	Leu	Val	
	130						135					140				
gaa	aaa	gct	aat	aca	gtt	gta	ggt	gct	tca	ctt	ttt	gta	aac	tgg	gta	480
Glu	Lys	Ala	Asn	Thr	Val	Val	Gly	Ala	Ser	Leu	Phe	Val	Asn	Trp	Val	
145					150					155				160		
aaa	gga	gta	ata	gat	gat	ttt	aca	tct	gaa	tcc	aca	caa	aaa	agt	act	528
Lys	Gly	Val	Ile	Asp	Asp	Phe	Thr	Ser	Glu	Ser	Thr	Gln	Lys	Ser	Thr	
				165					170					175		
ata	gat	aaa	gtt	tca	gat	gta	tcc	ata	att	att	ccc	tat	ata	gga	cct	576
Ile	Asp	Lys	Val	Ser	Asp	Val	Ser	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	
			180										190			
gct	ttg	aat	gta	gga	aat	gaa	aca	gct	aaa	gaa	aat	ttt	aaa	aat	gct	624
Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Glu	Asn	Phe	Lys	Asn	Ala	
		195					200					205				
ttt	gaa	ata	ggt	gga	gcc	gct	atc	tta	atg	gag	ttt	att	cca	gaa	ctt	672
Phe	Glu	Ile	Gly	Gly	Ala	Ala	Ile	Leu	Met	Glu	Phe	Ile	Pro	Glu	Leu	
	210					215					220					
att	gta	cct	ata	gtt	gga	ttt	ttt	aca	tta	gaa	tca	tat	gta	gga	aat	720
Ile	Val	Pro	Ile	Val	Gly	Phe	Phe	Thr	Leu	Glu	Ser	Tyr	Val	Gly	Asn	
225					230					235				240		
aaa	ggg	cat	att	att	atg	acg	ata	tcc	aat	gct	tta	aag	aaa	agg	gat	768
Lys	Gly	His	Ile	Ile	Met	Thr	Ile	Ser	Asn	Ala	Leu	Lys	Lys	Arg	Asp	
				245					250					255		
caa	aaa	tgg	aca	gat	atg	tat	ggt	ttg	ata	gta	tcg	cag	tgg	ctc	tca	816
Gln	Lys	Trp	Thr	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ser	Gln	Trp	Leu	Ser	
			260						265				270			
acg	gtt	aat	act	caa	ttt	tat	aca	ata	aaa	gaa	aga	atg	tac	aat	gct	864
Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Arg	Met	Tyr	Asn	Ala	
		275					280					285				
tta	aat	aat	caa	tca	caa	gca	ata	gaa	aaa	ata	ata	gaa	gat	caa	tat	912
Leu	Asn	Asn	Gln	Ser	Gln	Ala	Ile	Glu	Lys	Ile	Ile	Glu	Asp	Gln	Tyr	
	290					295					300					
aat	aga	tat	agt	gaa	gaa	gat	aaa	atg	aat	att	aac	att	gat	ttt	aat	960
Asn	Arg	Tyr	Ser	Glu	Glu	Asp	Lys	Met	Asn	Ile	Asn	Ile	Asp	Phe	Asn	
305					310					315				320		

gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat	1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn	
325 330 335	
ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga	1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg	
340 345 350	
atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt	1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu	
355 360 365	
aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt	1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu	
370 375 380	
gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac	1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp	
385 390 395 400	
agt ata cca ttt gat ctt tca cta tat acc taa	1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr	
405 410	

<210> 32

<211> 410

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 32

Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn	
1 5 10 15	
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu	
20 25 30	
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu	
35 40 45	
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser	
50 55 60	
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp	
65 70 75 80	
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile	
85 90 95	
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe	
100 105 110	
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala	
115 120 125	
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val	
130 135 140	
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val	
145 150 155 160	
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr	
165 170 175	

Ile	Asp	Lys	Val	Ser	Asp	Val	Ser	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro
		180						185					190		
Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Glu	Asn	Phe	Lys	Asn	Ala
		195						200					205		
Phe	Glu	Ile	Gly	Gly	Ala	Ala	Ile	Leu	Met	Glu	Phe	Ile	Pro	Glu	Leu
		210				215						220			
Ile	Val	Pro	Ile	Val	Gly	Phe	Phe	Thr	Leu	Glu	Ser	Tyr	Val	Gly	Asn
225					230					235					240
Lys	Gly	His	Ile	Ile	Met	Thr	Ile	Ser	Asn	Ala	Leu	Lys	Lys	Arg	Asp
				245					250						255
Gln	Lys	Trp	Thr	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ser	Gln	Trp	Leu	Ser
				260				265						270	
Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Arg	Met	Tyr	Asn	Ala
		275					280						285		
Leu	Asn	Asn	Gln	Ser	Gln	Ala	Ile	Glu	Lys	Ile	Ile	Glu	Asp	Gln	Tyr
		290				295					300				
Asn	Arg	Tyr	Ser	Glu	Glu	Asp	Lys	Met	Asn	Ile	Asn	Ile	Asp	Phe	Asn
305					310					315					320
Asp	Ile	Asp	Phe	Lys	Leu	Asn	Gln	Ser	Ile	Asn	Leu	Ala	Ile	Asn	Asn
				325					330					335	
Ile	Asp	Asp	Phe	Ile	Asn	Gln	Cys	Ser	Ile	Ser	Tyr	Leu	Met	Asn	Arg
			340					345					350		
Met	Ile	Pro	Leu	Ala	Val	Lys	Lys	Leu	Lys	Asp	Phe	Asp	Asp	Asn	Leu
		355					360					365			
Lys	Arg	Asp	Leu	Leu	Glu	Tyr	Ile	Asp	Thr	Asn	Glu	Leu	Tyr	Leu	Leu
	370				375						380				
Asp	Glu	Val	Asn	Ile	Leu	Lys	Ser	Lys	Val	Asn	Arg	His	Leu	Lys	Asp
385				390						395					400
Ser	Ile	Pro	Phe	Asp	Leu	Ser	Leu	Tyr	Thr						
			405						410						

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<221> CDS
 <222> (10)...(1305)

<400> 33
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 Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
 1 5 10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac 99
 Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15 20 25 30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct 147
 Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
 35 40 45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt 195

Ile	Asn	Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly		
			50					55					60				
atc	tac	tct	tct	aaa	ccg	tct	gaa	gta	aac	atc	gct	cag	aac	aac	gac	243	
Ile	Tyr	Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp		
		65					70				75						
atc	atc	tac	aac	ggc	cgt	tac	cag	aac	ttc	tct	atc	tct	ttc	tgg	gtt	291	
Ile	Ile	Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val		
	80					85				90							
cgt	atc	ccg	aaa	tac	ttc	aac	aaa	gtt	aac	ctg	aac	aac	gaa	tac	act	339	
Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr		
	95				100					105					110		
atc	atc	gac	tgc	atc	cgt	aac	aac	aac	tct	ggc	tgg	aaa	atc	tct	ctg	387	
Ile	Ile	Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu		
			115						120					125			
aac	tac	aac	aaa	atc	atc	tgg	act	ctg	cag	gac	act	gct	ggc	aac	aac	435	
Asn	Tyr	Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn		
			130					135					140				
cag	aaa	ctg	gtt	ttc	aac	tac	act	cag	atg	atc	tct	atc	tct	gac	tac	483	
Gln	Lys	Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr		
		145					150					155					
att	aac	aaa	tgg	atc	ttc	gtt	act	atc	act	aac	aac	cgt	ctg	ggc	aac	531	
Ile	Asn	Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn		
	160					165					170						
tct	cgt	atc	tac	atc	aac	ggc	aac	ctg	atc	gat	gaa	aaa	tct	atc	tct	579	
Ser	Arg	Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser		
	175				180					185					190		
aac	ctg	ggc	gac	atc	cac	gtt	tct	gac	aac	atc	ctg	ttc	aaa	atc	gtt	627	
Asn	Leu	Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val		
			195					200						205			
ggc	tgc	aac	gac	acg	cgt	tac	gtt	ggc	atc	cgt	tac	ttc	aaa	gtt	ttc	675	
Gly	Cys	Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe		
			210					215					220				
gac	act	gaa	ctg	ggc	aaa	act	gaa	atc	gaa	act	ctg	tac	tct	gac	gaa	723	
Asp	Thr	Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu		
		225					230					235					
ccg	gac	ccg	tct	atc	ctg	aaa	gac	ttc	tgg	ggc	aac	tac	ctg	ctg	tac	771	
Pro	Asp	Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr		
	240					245					250						
aac	aaa	cgt	tac	tac	ctg	ctg	aac	ctg	ctc	cgg	act	gac	aaa	tct	atc	819	
Asn	Lys	Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile		
	255				260				265						270		
act	cag	aac	tct	aac	ttc	ctg	aac	atc	aac	cag	cag	cgt	ggc	gtt	tat	867	
Thr	Gln	Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr		

275	280	285	
cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa			915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu			
290	295	300	
gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac			963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn			
305	310	315	
ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac			1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp			
320	325	330	
gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa			1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys			
335	340	345	350
atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag			1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln			
355	360	365	
atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag			1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln			
370	375	380	
aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac			1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn			
385	390	395	
ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct			1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser			
400	405	410	
tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag			1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln			
415	420	425	430
gaa aac taagaattc			1314
Glu Asn			

<210> 34

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 34

Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu			
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Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn			
20	25	30	
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn			

		35				40				45					
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55				60					
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70					75				80	
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
				85				90					95		
Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
	115					120					125				
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150					155					160
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165					170					175		
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
	180							185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
	195					200					205				
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230					235					240
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245					250					255		
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
		260						265					270		
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
	275					280					285				
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305					310					315					320
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325					330					335		
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
		340						345					350		
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
	355					360					365				
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370					375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390					395					400
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn
			405						410				415		
Gly	Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn
			420					425					430		